



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of

Shibin Zhou *et al.*

Serial No. Unassigned

Filed: February 7, 2001

For: HUMAN FAST-1 GENE

)
) Prior Group Art Unit: 1636
)
) Prior Examiner: T. McKelvey
)
)
) Atty. Dkt. No. 01107.00087

SEQUENCE RULES COMPLIANCE

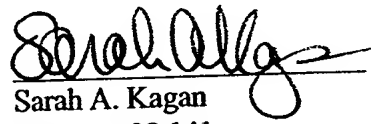
Assistant Commissioner of Patents & Trademarks
Washington, D.C. 20231

Dear Sir:

A paper copy of a substitute sequence listing submitted in parent application U.S. Serial No. 09/113,, 309 is submitted herewith. Please use the computer readable form submitted in the parent application on 18 November 1999 for examination of the subject application. The content of the two forms, paper and CRF, are believed to be identical.

Respectfully submitted,

02-06-01
Date


Sarah A. Kagan
Reg. No. 32,141

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COPY



SEQUENCE LISTING

<110> Zhou, Shibin
Zawel, Leigh
Vogelstein, Bert
Kinzler, Kenneth

<120> Human Fast-1 Gene

<130> 01107.10898

<140> 09/113,309

<141> 1998-07-10

<160> 19

<170> FastSEQ for Windows Version 3.0

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<212> DNA

<213> Homo sapiens

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35 40 45
Ala Pro Ser Arg Arg Leu Lys Leu Ala Gln Ile Ile Arg Gln Val Gln
50 55 60
Ala Val Phe Pro Phe Phe Arg Glu Asp Tyr Glu Gly Trp Lys Asp Ser
65 70 75 80
Ile Arg His Asn Leu Ser Ser Asn Arg Cys Phe Arg Lys Val Pro Lys
85 90 95
Asp Pro Ala Lys Pro Gln Ala Lys Gly Asn Phe Trp Ala Val Asp Val
100 105 110
Ser Leu Ile Pro Ala Glu Ala Leu Arg Leu Gln Asn Thr Ala Leu Cys
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Arg Arg Trp Gln Asn Gly Gly Ala Arg Gly Ala Phe Ala Lys Asp Leu
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Gly Pro Tyr Val Leu His Gly Arg Pro Tyr Arg Pro Pro Ser Pro Pro
145 150 155 160
Pro Pro Pro Ser Glu Gly Phe Ser Ile Lys Ser Leu Leu Gly Gly Ser
165 170 175
Gly Glu Gly Ala Pro Trp Pro Gly Leu Ala Pro Gln Ser Ser Pro Val
180 185 190
Pro Ala Gly Thr Gly Asn Ser Gly Glu Glu Ala Val Pro Thr Pro Pro
195 200 205
Leu Pro Ser Ser Glu Arg Pro Leu Trp Pro Leu Cys Pro Leu Pro Gly
210 215 220
Pro Thr Arg Val Glu Gly Glu Thr Val Gln Gly Gly Ala Ile Gly Pro
225 230 235 240
Ser Thr Leu Ser Pro Glu Pro Arg Ala Trp Pro Leu His Leu Leu Gln
245 250 255
Gly Thr Ala Val Pro Gly Gly Arg Ser Ser Gly Gly His Arg Ala Ser
260 265 270
Leu Trp Gly Gln Leu Pro Thr Ser Tyr Leu Pro Ile Tyr Thr Pro Asn
275 280 285
Val Val Met Pro Leu Ala Pro Pro Pro Thr Ser Cys Pro Gln Cys Pro
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Pro Gly Leu Leu Cys Asp Leu Asp Ala Leu Phe Gln Gly Val Pro Pro
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Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Cys
65 70 75 80
Asn Thr Lys Cys Val Thr Ile Pro Ser Thr Cys Ser Glu Ile Trp Gly
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Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp Asp Thr Thr Gly Leu Tyr
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Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp Gly Arg Leu Gln Val Ser
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His Arg Lys Gly Leu Pro His Val Ile Tyr Cys Arg Leu Trp Arg Trp
130 135 140
Pro Asp Leu His Ser His His Glu Leu Lys Ala Ile Glu Asn Cys Glu
145 150 155 160
Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val Cys Val Asn Pro Tyr His
165 170 175
Tyr Gln Arg Val Glu Thr Pro Val Leu Pro Pro Val Leu Val Pro Arg
180 185 190
His Thr Glu Ile Leu Thr Glu Leu Pro Pro Leu Asp Asp Tyr Thr His
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Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro Gln Ser
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Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly Tyr Ile Ser Glu Asp Gly
225 230 235 240
Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser Met Asp Thr Gly Ser Pro
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Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro Val Asn His Ser Leu Asp
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Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr Phe His Ala Ser Gln
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305 310 315 320
Phe Cys Leu Gly Leu Ser Asn Val Asn Arg Asn Ala Thr Val Glu
325 330 335
Met Thr Arg Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly
340 345 350
Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln
355 360 365
Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys
370 375 380
Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe
385 390 395 400
Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly Phe Glu Ala Val Tyr
405 410 415
Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp
420 425 430
Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser Thr Pro Cys Trp Ile
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 35 40 45
 Gln Pro Trp Pro Gln Pro Trp Pro Pro Leu Ser Leu Tyr Arg Glu Gly
 50 55 60
 Gly Thr Trp Ser Pro Asp Arg Gly Ser Met Tyr Gly Leu Ser Pro Gly
 65 70 75 80
 Thr His Glu Gly Ser Cys Thr His Thr His Glu Gly Pro Lys Asp Ser
 85 90 95
 Met Ala Gly Asp His Thr Arg Ser Arg Lys Ser Lys Lys Lys Asn Tyr
 100 105 110
 His Arg Tyr Tyr Lys Pro Pro Tyr Ser Tyr Leu Ala Met Ile Ala Leu
 115 120 125
 Val Ile Gln Asn Ser Pro Glu Lys Arg Leu Lys Leu Ser Gln Ile Leu
 130 135 140
 Lys Glu Val Ser Thr Leu Phe Pro Phe Phe Asn Gly Asp Tyr Met Gly
 145 150 155 160
 Trp Lys Asp Ser Ile Arg His Asn Leu Ser Ser Ser Asp Cys Phe Lys
 165 170 175
 Lys Ile Leu Lys Asp Pro Gly Lys Pro Gln Ala Lys Gly Asn Phe Trp
 180 185 190
 Thr Val Asp Val Ser Arg Ile Pro Leu Asp Ala Met Lys Leu Gln Asn
 195 200 205
 Thr Ala Leu Thr Arg Gly Gly Ser Asp Tyr Phe Val Gln Asp Leu Ala
 210 215 220
 Pro Tyr Ile Leu His Asn Tyr Lys Tyr Glu His Asn Ala Gly Ala Tyr
 225 230 235 240
 Gly His Gln Met Pro Pro Ser His Ala Arg Ser Leu Ser Leu Ala Glu
 245 250 255
 Asp Ser Gln Gln Thr Asn Thr Gly Gly Lys Leu Asn Thr Ser Phe Met
 260 265 270
 Ile Asp Ser Leu Leu His Asp Leu Gln Glu Val Asp Leu Pro Asp Ala
 275 280 285
 Ser Arg Asn Leu Glu Asn Gln Arg Ile Ser Pro Ala Val Ala Met Asn
 290 295 300
 Asn Met Trp Ser Ser Ala Pro Leu Leu Tyr Thr His Ser Lys Pro Thr
 305 310 315 320
 Arg Asn Ala Arg Ser Pro Gly Leu Ser Thr Ile His Ser Thr Tyr Ser
 325 330 335
 Ser Ser Ser Ser Ser Ile Ser Thr Ile Ser Pro Val Gly Phe Gln Lys
 340 345 350
 Glu Gln Glu Lys Ser Gly Arg Gln Thr Gln Arg Val Gly His Pro Ile

355 360 365
 Lys Arg Ser Arg Glu Asp Asp Asp Cys Ser Thr Thr Ser Ser Asp Pro
 370 375 380
 Asp Thr Gly Asn Tyr Ser Pro Ile Glu Pro Pro Lys Lys Met Pro Leu
 385 390 395 400
 Leu Ser Leu Asp Leu Pro Thr Ser Tyr Thr Lys Ser Val Ala Pro Asn
 405 410 415
 Val Val Ala Pro Pro Ser Val Leu Pro Phe Phe His Phe Pro Arg Phe
 420 425 430
 Thr Tyr Tyr Asn Tyr Gly Pro Ser Pro Tyr Met Thr Pro Pro Tyr Trp
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 Gly Phe Pro His Pro Thr Asn Ser Gly Gly Asp Ser Pro Arg Gly Pro
 450 455 460
 Gln Ser Pro Leu Asp Leu Asp Asn Met Leu Arg Ala Met Pro Pro Asn
 465 470 475 480
 Lys Ser Val Phe Asp Val Leu Thr Ser His Pro Gly Asp Leu Val His
 485 490 495
 Pro Ser Phe Leu Ser Gln Cys Leu Gly Ser Ser Gly Ser Pro Tyr Pro
 500 505 510
 Ser Arg Gln Gly Leu Met
 515



FIG. 1

hFAST-1	hpcsgsrllgpeaespsqp-----	21
xFAST-1	hdpsslysgnpgsqyesvepsslallssidqeqlpvatgqsynhsvqpw	51
hFAST-1	-----	21
xFAST-1	pqpwpplsllyreggtwspdrsgmyglspgthegscththegpkdsmagdht	102
hFAST-1	---KRRKKRYLHDKPPYITLAMIATLVIAAPSRRLKLAQITIRQVQAVFPF	69
xFAST-1	rsrKSKKKNYHNYKPPYSYLAAMIATLVIONSPKRLKLSQILKEVSTLFPF	153
hFAST-1	FREDYEGWKDSTRHNLSSNRCHKVPKDPAPQAKGNFWMDVSLIIPAEAL	120
xFAST-1	FNGDYMGWKDSTRHNLSSDCFKKILKDPGKPOAKGNFWMDVSRNIPLDAM	204
hFAST-1	RLONTALCRwqngGARGAFKDLGPYVLHGRPYrppspppppsegfsjks	171
xFAST-1	KLONTALTR-----GGSDYFVQDLAPYILLHNYKVEhnagayghqmpshar	250
hFAST-1	llggsggapwpglapqssypagtgnsgeeavtpplpsserplwplcpl	222
xFAST-1	slslaedsqqtntggklntsfmidsllhdldqevdlldasrnlengrispav	301
hFAST-1	pgptrvegetvqggaigstlspeprawlhlqgtavpggrssgghrasl	273
xFAST-1	amnmwssaplllythskptrnarsoglstihstysssssstistispvgfqk	352
hFAST-1	wgq-----	276
xFAST-1	eqeksgqrtqrvgpikrsreddcsttssdpdtgnyspieppkmpllsl	403
hFAST-1	-LPTSLPIYTPNVVMPlapptscpcqpcstspaywgvapetrpgpgllc-	325
xFAST-1	dLPTSMTKSVAPNVVAPsvlghfhfrfyyngpspymtppywgfphpt	454
hFAST-1	-----DLDAFGQVPPMKSTYDMVSHPRDLAAPpggwllsw	362
xFAST-1	nsggdsprgqpqlDLNMLRAMPNKSVMLTSHPGDLVHPSflsqclg	505
hFAST-1	csll-----	365
xFAST-1	ssgspysrqglm	518



FIG. 2A

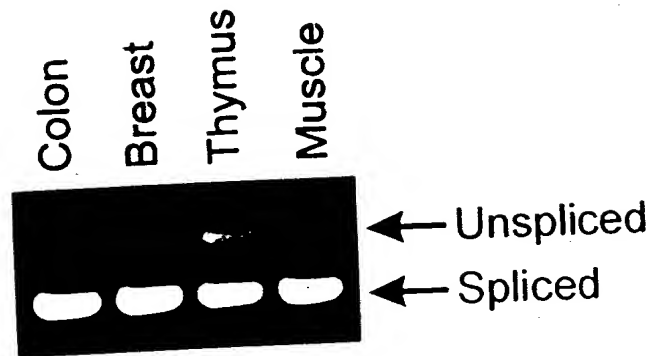


FIG. 2B

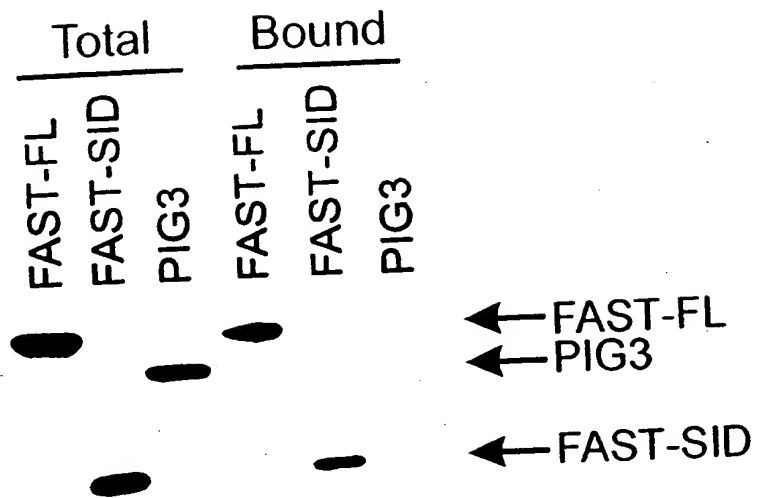




FIG. 3A

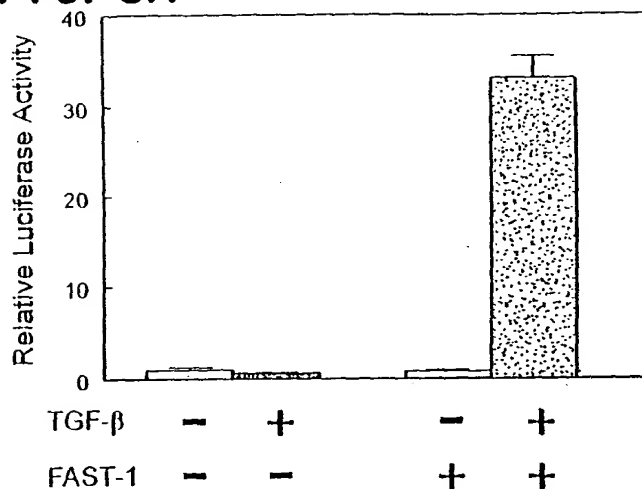


FIG. 3B

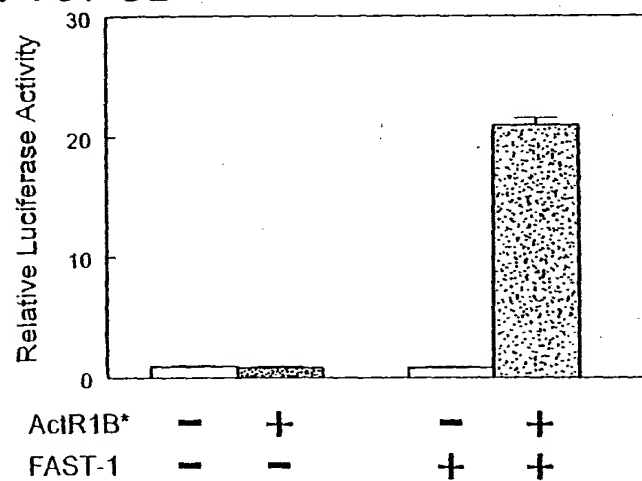


FIG. 3C

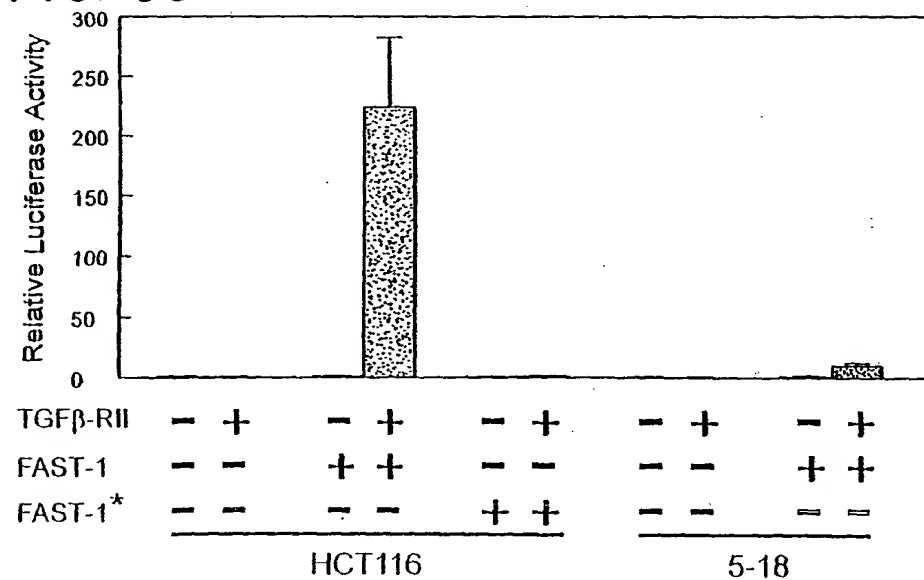




FIG. 4A

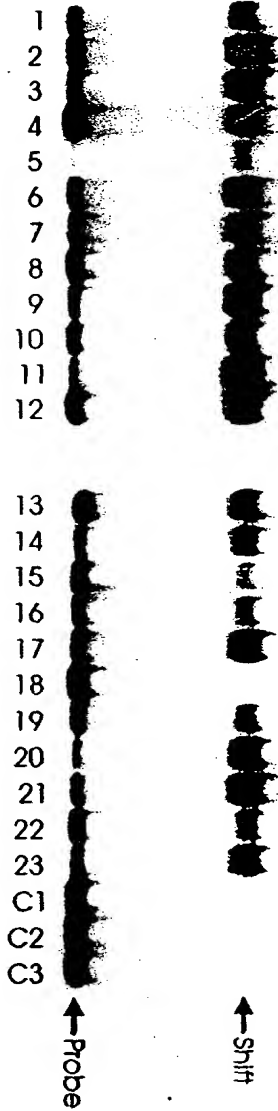


FIG. 4B

	FAST-FL				FAST-FH				FAST-FL				FAST-FH				FAST-FL				FAST-FH			
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FIG. 4C

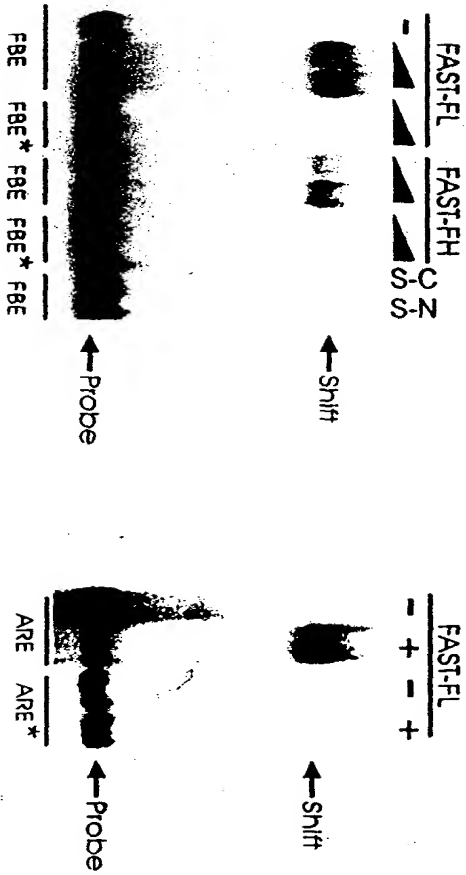


FIG. 4D

